

318



OIPE

2  
ENTERED

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/075,846

DATE: 03/01/2002 P.5  
 TIME: 11:50:04

Input Set : A:\EP.txt  
 Output Set: N:\CRF3\03012002\J075846.raw

3 <110> APPLICANT: Bristol-Myers Squibb Company  
 5 <120> TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA  
 SUBUNIT EXPRESSED  
 6 IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREOF  
 8 <130> FILE REFERENCE: D0079 NP  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/075,846.  
 C--> 10 <141> CURRENT FILING DATE: 2002-02-13  
 10 <150> PRIOR APPLICATION NUMBER: US 60/269,535  
 11 <151> PRIOR FILING DATE: 2001-02-16  
 13 <160> NUMBER OF SEQ ID NOS: 81  
 15 <170> SOFTWARE: PatentIn version 3.0  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 2565  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: homo sapiens  
 22 <220> FEATURE:  
 23 <221> NAME/KEY: CDS  
 24 <222> LOCATION: (1)..(1251)  
 26 <400> SEQUENCE: 1  
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 28 Met Thr Thr Leu Val Pro Ala Thr Leu Ser Phe Leu Leu Leu Trp Thr  
 29 1 5 10 15  
 31 ctg cca ggg cag gtc ctc ctc agg gtg gcc ttg gca aaa gag gaa gtc 96  
 32 Leu Pro Gly Gln Val Leu Leu Arg Val Ala Leu Ala Lys Glu Glu Val  
 33 20 25 30  
 35 aaa tct gga acc aag ggg tcc cag ccc atg tcc ccc tct gat ttc cta 144  
 36 Lys Ser Gly Thr Lys Gly Ser Gln Pro Met Ser Pro Ser Asp Phe Leu  
 37 35 40 45  
 39 gac aaa ctt atg ggg cga aca tct gga tat gat gcc agg att cgg ccc 192  
 40 Asp Lys Leu Met Gly Arg Thr Ser Gly Tyr Asp Ala Arg Ile Arg Pro  
 41 50 55 60  
 43 aat ttt aaa ggc cca ccc gtg aac gtg acc tgc aac atc ttc atc aac 240  
 44 Asn Phe Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn  
 45 65 70 75 80  
 47 agt ttc agc tcc gtc acc aag acc aca atg gac tac cgg gtg aat gtc 288  
 48 Ser Phe Ser Ser Val Thr Lys Thr Met Asp Tyr Arg Val Asn Val  
 49 85 90 95  
 51 ttc ttg cgg caa cag tgg aat gac cca cgc ctg tcc tac cga gaa tat 336  
 52 Phe Leu Arg Gln Gln Trp Asn Asp Pro Arg Leu Ser Tyr Arg Glu Tyr  
 53 100 105 110  
 55 cct gat gac tct ctg gac ctc gat ccc tcc atg ctg gac tct atc tgg 384  
 56 Pro Asp Asp Ser Leu Asp Leu Asp Pro Ser Met Leu Asp Ser Ile Trp  
 57 115 120 125  
 59 aag cca gac ctc ttc ttt gct aat gag aaa ggg gcc aac ttc cat gag 432

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60	Lys Pro Asp Leu Phe Phe Ala Asn Glu Gly Ala Asn Phe His Glu			
61	130	135	140	
63	gtg acc acg gac aac aac aag tta ctg cgc atc ttc aag aat ggg aat gtg	480		
64	Val Thr Thr Asp Asn Lys Leu Leu Arg Ile Phe Lys Asn Gly Asn Val			
65	145	150	155	160
67	ctg tac agc atc agg ctg acc ctc att ttg tcc tgc ctg atg gac ctc	528		
68	Leu Tyr Ser Ile Arg Leu Thr Leu Ile Leu Ser Cys Leu Met Asp Leu			
69	165	170	175	
71	aag aac ttc ccc atg gac atc cag acc tgc acg atg cag ctt gag agc	576		
72	Lys Asn Phe Pro Met Asp Ile Gln Thr Cys Thr Met Gln Leu Glu Ser			
73	180	185	190	
75	ttt ggc tac acc atg aaa gac ctc gtg ttt gag tgg ctg gaa gat gct	624		
76	Phe Gly Tyr Thr Met Lys Asp Leu Val Phe Glu Trp Leu Glu Asp Ala			
77	195	200	205	
79	cct gct gtc caa gtg gct gag ggg ctg act ctg ccc cag ttt atc ttg	672		
80	Pro Ala Val Gln Val Ala Glu Gly Leu Thr Leu Pro Gln Phe Ile Leu			
81	210	215	220	
83	cgg gat gag aag gat cta ggc tgt tgt acc aag cac tac aac aca ggg	720		
84	Arg Asp Glu Lys Asp Leu Gly Cys Cys Thr Lys His Tyr Asn Thr Gly			
85	225	230	235	240
87	aaa ttc acc tgc atc gag gta aag ttt cac ctg gaa cgg cag atg ggc	768		
88	Lys Phe Thr Cys Ile Glu Val Lys Phe His Leu Glu Arg Gln Met Gly			
89	245	250	255	
91	tac tat ctg att cag atg tac atc ccc agc cta ctc atc gtc atc ctg	816		
92	Tyr Tyr Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile Val Ile Leu			
93	260	265	270	
95	tcc tgg gtc tcc ttc tgg atc aac atg gat gct gcc cct gcc cgt gtg	864		
96	Ser Trp Val Ser Phe Trp Ile Asn Met Asp Ala Ala Pro Ala Arg Val			
97	275	280	285	
99	ggc ctg ggc atc acc acc gtg ctc acc atg acc acc cag agc tct ggc	912		
100	Gly Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser Ser Gly			
101	290	295	300	
103	tcc cgg gcc tct ttg cct aag gtg tcc tac gtg aag gca atc gac atc	960		
104	Ser Arg Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala Ile Asp Ile			
105	305	310	315	320
107	tgg atg gct gtg tgt ctg ctc ttt gtg ttc gct gcc ttg ctg gag tat	1008		
108	Trp Met Ala Val Cys Leu Leu Phe Val Phe Ala Ala Leu Leu Glu Tyr			
109	325	330	335	
111	gct gcc ata aat ttt gtt tct cgt cag cat aaa gaa ttc ata cga ctt	1056		
112	Ala Ala Ile Asn Phe Val Ser Arg Gln His Lys Glu Phe Ile Arg Leu			
113	340	345	350	
115	cga aga agg cag agg cgc caa cgc ttg gag gaa gat atc atc caa gaa	1104		
116	Arg Arg Arg Gln Arg Arg Gln Arg Leu Glu Glu Asp Ile Ile Gln Glu			
117	355	360	365	
119	agt cgt ttc tat ttc cgt ggc tat ggc ttg ggc cac tgc ctg cag gca	1152		
120	Ser Arg Phe Tyr Phe Arg Gly Tyr Gly Leu Gly His Cys Leu Gln Ala			
121	370	375	380	
123	aga gat gga ggt cca atg gaa ggt tct ggc att tat agt ccc caa cct	1200		
124	Arg Asp Gly Gly Pro Met Glu Gly Ser Gly Ile Tyr Ser Pro Gln Pro			

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125	385	390	395	400	
127	cca gcc cct ctt cta agg gaa gga gaa acc acg	cg	aaa ctc tac	gtg	1248
128	Pro Ala Pro Leu Leu Arg Glu Gly Glu	Thr Thr Arg Lys	Leu Tyr Val		
129	405		410	415	
131	gac tgagccaaga gaattgacac catctccgg	gctgtcttcc	ctttcacttt		1301
132	Asp				
135	cctcatcttc aatatcttct actgggttgt ctataaagtgc	tacggtcag	aagatatcca		1361
137	ccaggctctg tgaatagggt gggagctata gagtcctgtct	gctggcctcc	tgcttcctcc		1421
139	tgggtgggt ttctccctca gtttagactcc attaggggtt	tggacagttc	cttcctgtatc		1481
141	tcccactca aacttcaact accagtccca aagctatgtg	ggccttatatt	gcatggtgc		1541
143	aatgggtggct gtacttataa agatggctta tctaccctag	tccatatttt	ctccataactt		1601
145	tcaccatttct catgagacta aggtttggcc acattcctgg	ggccaggatg	accttctgc		1661
147	cttgctggag cttccctgtt ttccaataact ccagtggaga	gtattcagaa	cactgctgt		1721
149	agattctggc atttgcatac ttaatctgca ccacttctcc	ccctgccacc	tcccacccag		1781
151	agcctggcca ttactctgtc ctctgtccct cctgtgcag	attcaaatgg	tgagtttctc		1841
153	ctatccacaa gtgctccct gtggggcccta gtcaggtttc	cttgaagtga	gaggaaggca		1901
155	aagccgcaag ttccccacct. ctcgagaggg ttggAACAGT	cataggctgc	actggctag		1961
157	cgaactatatg gcccacaga gaggtttca agtctttgg	gaagccccac	actttgttct		2021
159	catccctttt cctattgcgc ttgtctgtc ttccctgttc	actgagatac	tcctctgtc		2081
161	tgtctcttag ttttgaggag aycgttctga gctgaccagg	gtagctggtt	cagaaattac		2141
163	tgtcagaatt gggcagaga ctttgggttc tcaaaaagac	taaccttcca	gatccacctg		2201
165	aacattctgg ttcagaaat attcgttccg ttccctaatt	aactagcatg	gtggcaggat		2261
167	ctgttggaca gctggggagt gtaaaaaaaag aaaaatactt	gttctttaag	aaacttactt		2321
169	tatgatgcta gaaaactttt gagaaaaagtg agatccaagg	tagtggaaacc	caggaggagt		2381
171	agaatagaga aactattctc agagtgtctt ttgttggctg	ggcttcatt	tgtttcttct		2441
173	ttctcaccaa agtctatttt ccagggccct tcatttccaa	cctggcttt	cacctcctt		2501
175	tgggtgc当地 ataaagggtgc cgctgcaacc ttgttaagga	taaaaaaaaaa	aaaaaaaaaa		2561
177	aaaa				2565
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181	<211> LENGTH: 417				
182	<212> TYPE: PRT				
183	<213> ORGANISM: homo sapiens				
185	<400> SEQUENCE: 2				
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192	20	25	30		
195	Lys Ser Gly Thr Lys Gly Ser Gln Pro Met Ser Pro Ser Asp Phe Leu				
196	35	40	45		
199	Asp Lys Leu Met Gly Arg Thr Ser Gly Tyr Asp Ala Arg Ile Arg Pro				
200	50	55	60		
203	Asn Phe Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn				
204	65	70	75	80	
207	Ser Phe Ser Ser Val Thr Lys Thr Thr Met Asp Tyr Arg Val Asn Val				
208	85	90	95		
211	Phe Leu Arg Gln Gln Trp Asn Asp Pro Arg Leu Ser Tyr Arg Glu Tyr				
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215	Pro Asp Asp Ser Leu Asp Leu Asp Pro Ser Met Leu Asp Ser Ile Trp				
216	115	120	125		

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219 Lys Pro Asp Leu Phe Phe Ala Asn Glu Lys Gly Ala Asn Phe His Glu  
220 130 135 140  
223 Val Thr Thr Asp Asn Lys Leu Leu Arg Ile Phe Lys Asn Gly Asn Val  
224 145 150 155 160  
227 Leu Tyr Ser Ile Arg Leu Thr Leu Ile Leu Ser Cys Leu Met Asp Leu  
228 165 170 175  
231 Lys Asn Phe Pro Met Asp Ile Gln Thr Cys Thr Met Gln Leu Glu Ser  
232 180 185 190  
235 Phe Gly Tyr Thr Met Lys Asp Leu Val Phe Glu Trp Leu Glu Asp Ala  
236 195 200 205  
239 Pro Ala Val Gln Val Ala Glu Gly Leu Thr Leu Pro Gln Phe Ile Leu  
240 210 215 220  
243 Arg Asp Glu Lys Asp Leu Gly Cys Cys Thr Lys His Tyr Asn Thr Gly  
244 225 230 235 240  
247 Lys Phe Thr Cys Ile Glu Val Lys Phe His Leu Glu Arg Gln Met Gly  
248 245 250 255  
251 Tyr Tyr Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile Val Ile Leu  
252 260 265 270  
255 Ser Trp Val Ser Phe Trp Ile Asn Met Asp Ala Ala Pro Ala Arg Val  
256 275 280 285  
259 Gly Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser Ser Gly  
260 290 295 300  
263 Ser Arg Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala Ile Asp Ile  
264 305 310 315 320  
267 Trp Met Ala Val Cys Leu Leu Phe Val Phe Ala Ala Leu Leu Glu Tyr  
268 325 330 335  
271 Ala Ala Ile Asn Phe Val Ser Arg Gln His Lys Glu Phe Ile Arg Leu  
272 340 345 350  
275 Arg Arg Arg Gln Arg Arg Gln Arg Leu Glu Glu Asp Ile Ile Gln Glu  
276 355 360 365  
279 Ser Arg Phe Tyr Phe Arg Gly Tyr Gly Leu Gly His Cys Leu Gln Ala  
280 370 375 380  
283 Arg Asp Gly Gly Pro Met Glu Gly Ser Gly Ile Tyr Ser Pro Gln Pro  
284 385 390 395 400  
287 Pro Ala Pro Leu Leu Arg Glu Gly Glu Thr Thr Arg Lys Leu Tyr Val  
288 405 410 415  
291 Asp  
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296 <211> LENGTH: 1640  
297 <212> TYPE: DNA  
298 <213> ORGANISM: homo sapiens  
300 <220> FEATURE:  
301 <221> NAME/KEY: CDS  
302 <222> LOCATION: (1)..(1293)  
304 <400> SEQUENCE: 3  
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306 Met Thr Thr Leu Val Pro Ala Thr Leu Ser Phe Leu Leu Leu Trp Thr  
307 1 5 10 15  
309 ctg cca ggg cag gtc ctc ctc agg gtg gcc ttg gca aaa gag gaa gtc 96

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310	Leu	Pro	Gly	Gln	Val	Leu	Leu	Arg	Val	Ala	Leu	Ala	Lys	Glu	Glu	Val
311					20				25				30			
313	aaa	tct	gga	acc	aag	ggg	tcc	cag	ccc	atg	tcc	ccc	tct	gat	ttc	cta
314	Lys	Ser	Gly	Thr	Lys	Gly	Ser	Gln	Pro	Met	Ser	Pro	Ser	Asp	Phe	Leu
315					35				40				45			
317	gac	aaa	ctt	atg	ggg	cga	aca	tct	gga	tat	gat	gcc	agg	att	cgg	ccc
318	Asp	Lys	Leu	Met	Gly	Arg	Thr	Ser	Gly	Tyr	Asp	Ala	Arg	Ile	Arg	Pro
319					50				55				60			
321	aat	ttt	aaa	ggc	cca	ccc	gtg	aac	gtg	acc	tgc	aac	atc	ttc	atc	aac
322	Asn	Phe	Lys	Gly	Pro	Pro	Val	Asn	Val	Thr	Cys	Asn	Ile	Phe	Ile	Asn
323					65				70				75			80
325	agt	ttc	agc	tcc	gtc	acc	aag	acc	aca	atg	gac	tac	cgg	gtg	aat	gtc
326	Ser	Phe	Ser	Ser	Val	Thr	Lys	Thr	Thr	Met	Asp	Tyr	Arg	Val	Asn	Val
327					85				90				95			
329	ttc	ttg	cgg	caa	cag	tgg	aat	gac	cca	cgc	ctg	tcc	tac	cga	gaa	tat
330	Phe	Leu	Arg	Gln	Gln	Trp	Asn	Asp	Pro	Arg	Leu	Ser	Tyr	Arg	Glu	Tyr
331					100				105				110			
333	cct	gat	gac	tct	ctg	gac	ctc	gat	ccc	tcc	atg	ctg	gac	tct	atc	tgg
334	Pro	Asp	Asp	Ser	Leu	Asp	Leu	Asp	Pro	Ser	Met	Leu	Asp	Ser	Ile	Trp
335					115				120				125			
337	aag	cca	gac	ctc	tcc	ttt	gct	aat	gag	aaa	ggg	gcc	aac	ttc	cat	gag
338	Lys	Pro	Asp	Leu	Phe	Phe	Ala	Asn	Glu	Lys	Gly	Ala	Asn	Phe	His	Glu
339					130				135				140			
341	gtg	acc	acg	gac	aac	aag	tta	ctg	cgc	atc	ttc	aag	aat	ggg	aat	gtg
342	Val	Thr	Thr	Asp	Asn	Lys	Leu	Leu	Arg	Ile	Phe	Lys	Asn	Gly	Asn	Val
343					145				150				155			160
345	ctg	tac	agc	atc	agg	ctg	acc	ctc	att	ttg	tcc	tgc	ctg	atg	gac	ctc
346	Leu	Tyr	Ser	Ile	Arg	Leu	Thr	Leu	Ile	Leu	Ser	Cys	Leu	Met	Asp	Leu
347					165				170				175			
349	aag	aac	ttc	ccc	atg	gac	atc	cag	acg	tgc	acg	atg	cag	ctt	gag	agc
350	Lys	Asn	Phe	Pro	Met	Asp	Ile	Gln	Thr	Cys	Thr	Met	Gln	Leu	Glu	Ser
351					180				185				190			
353	tca	tcc	ata	ctc	tgc	agc	cct	ctg	cca	tct	ctg	tca	ctt	tca	gtt	ggc
354	Ser	Ser	Ile	Leu	Cys	Ser	Pro	Leu	Pro	Ser	Leu	Ser	Leu	Ser	Val	Gly
355					195				200				205			
357	tac	acc	atg	aaa	gac	ctc	gtg	ttt	gag	tgg	ctg	gaa	gat	gct	cct	gtc
358	Tyr	Thr	Met	Lys	Asp	Leu	Val	Phe	Glu	Trp	Leu	Glu	Asp	Ala	Pro	Ala
359					210				215				220			
361	gtc	caa	gtg	gct	gag	ggg	ctg	act	ctg	ccc	cag	ttt	atc	ttg	cgg	gtat
362	Val	Gln	Val	Ala	Glu	Gly	Leu	Thr	Leu	Pro	Gln	Phe	Ile	Leu	Arg	Asp
363					225				230				235			240
365	gag	aag	gat	cta	ggc	tgt	tgt	acc	aag	cac	tac	aac	aca	ggg	aaa	ttc
366	Glu	Lys	Asp	Leu	Gly	Cys	Cys	Thr	Lys	His	Tyr	Asn	Thr	Gly	Lys	Phe
367					245				250				255			
369	acc	tgc	atc	gag	gta	aag	ttt	cac	ctg	gaa	cgg	cag	atg	ggc	tac	tat
370	Thr	Cys	Ile	Glu	Val	Lys	Phe	His	Leu	Glu	Arg	Gln	Met	Gly	Tyr	Tyr
371					260				265				270			
373	ctg	att	cag	atg	tac	atc	ccc	agc	cta	ctc	atc	gtc	atc	ctg	tcc	tgg
374	Leu	Ile	Gln	Met	Tyr	Ile	Pro	Ser	Leu	Leu	Ile	Val	Ile	Leu	Ser	Trp

→ Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/075,846

DATE: 03/01/2002  
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:906 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12